



1

SEQUENCE LISTING

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DEC 12 2001

TECH CENTER 1600/2900

<110> Blundell, Tom L  
Abell, Christopher  
Inoue, Tsuyoshi  
von Delft, Frank

<120> Crystal Structure

<130> 620-139

<140> US 09/820,745

<141> 2001-03-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 1

Leu Val Gly Asp Ser Leu Gly Met

1

5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 2

Val Lys Ile Glu Gly Gly

1

5

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

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<220>  
<221> SITE  
<222> (3)  
<223> Xaa is a hydrophobic residue

<400> 3  
Gly His Xaa Gly Leu Thr Pro Gln  
1 5

<210> 4  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 4  
Gly Gly Tyr Lys Val Gln Gly  
1 5

<210> 5  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 5  
Ile Gly Ile Gly Ala Gly  
1 5

<210> 6  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 6  
Asp Gly Asn Ile Leu Val  
1 5

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<210> 7  
 <211> 264  
 <212> PRT  
 <213> Escherichia coli

<400> 7

Met Lys Pro Thr Thr Ile Ser Leu Leu Gln Lys Tyr Lys Gln Asp Lys  
 1 5 10 15

Lys Arg Phe Ala Thr Ile Thr Ala Tyr Asp Tyr Ser Phe Ala Lys Leu  
 20 25 30

Phe Ala Asp Glu Gly Leu Asn Val Met Leu Val Gly Asp Ser Leu Gly  
 35 40 45

Met Thr Val Gln Gly His Asp Ser Thr Leu Pro Val Thr Val Ala Asp  
 50 55 60

Ile Ala Tyr His Thr Ala Ala Val Arg Arg Gly Ala Pro Asn Cys Leu  
 65 70 75 80

Leu Leu Ala Asp Leu Pro Phe Met Ala Tyr Ala Thr Pro Glu Gln Ala  
 85 90 95

Phe Glu Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Met Val Lys  
 100 105 110

Ile Glu Gly Gly Glu Trp Leu Val Glu Thr Val Gln Met Leu Thr Glu  
 115 120 125

Arg Ala Val Pro Val Cys Gly His Leu Gly Leu Thr Pro Gln Ser Val  
 130 135 140

Asn Ile Phe Gly Gly Tyr Lys Val Gln Gly Arg Gly Asp Glu Ala Gly  
 145 150 155 160

Asp Gln Leu Leu Ser Asp Ala Leu Ala Leu Glu Ala Ala Gly Ala Gln  
 165 170 175

Leu Leu Val Leu Glu Cys Val Pro Val Glu Leu Ala Lys Arg Ile Thr  
 180 185 190

Glu Ala Leu Ala Ile Pro Val Ile Gly Ile Gly Ala Gly Asn Val Thr  
 195 200 205

Asp Gly Gln Ile Leu Val Met His Asp Ala Phe Gly Ile Thr Gly Gly  
 210 215 220

His Ile Pro Lys Phe Ala Lys Asn Phe Leu Ala Glu Thr Gly Asp Ile  
 225 230 235 240

Arg Ala Ala Val Arg Gln Tyr Met Ala Glu Val Glu Ser Gly Val Tyr  
 245 250 255

Pro Gly Glu Glu His Ser Phe His  
 260

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<210> 8  
 <211> 267  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 8

Met Ser Leu Lys Gln Ile Thr Ile Ser Thr Leu Arg Gln Trp Lys Leu  
 1 5 10 15

Ala Asn Lys Lys Phe Ala Cys Ile Thr Ala Tyr Asp Ala Ser Phe Ser  
 20 25 30

Arg Leu Phe Ala Glu Gln Gly Met Pro Val Met Leu Val Gly Asp Ser  
 35 40 45

Leu Gly Met Thr Ala Gln Gly His Ser Thr Thr Leu Pro Val Ser Val  
 50 55 60

Glu Asp Ile Ala Tyr His Thr Lys Ser Val Arg Arg Gly Ala Pro Asn  
 65 70 75 80

Arg Leu Leu Met Ala Asp Leu Pro Phe Met Ser Tyr Ser Thr Trp Glu  
 85 90 95

Asp Ala Cys Lys Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Ile  
 100 105 110

Val Lys Ile Glu Gly Gly Gly Asn Trp Ile Phe Glu Ile Val Gln Arg  
 115 120 125

Leu Thr Glu Arg Ser Val Pro Val Ala Gly His Leu Gly Leu Thr Pro  
 130 135 140

Gln Ser Val Asn Ile Phe Gly Gly Tyr Lys Ile Gln Gly Arg Glu Gln  
 145 150 155 160

Ser Ala Ala Ala Arg Leu Ile Glu Asn Ala Gln Gln Leu Glu Lys Phe  
 165 170 175

Gly Ala Gln Leu Leu Val Leu Glu Cys Ile Pro Glu Ser Leu Ala Glu  
 180 185 190

Gln Ile Thr Lys Thr Ile Ser Ile Pro Thr Ile Gly Ile Gly Ala Gly  
 195 200 205

Lys His Thr Asp Gly Gln Ile Leu Val Met His Asp Ala Leu Gly Ile  
 210 215 220

Thr Gly Gly Arg Pro Pro Lys Phe Ala Lys Asn Phe Leu Ser Gly Ala  
 225 230 235 240

Gly Asp Ile Arg Thr Ala Ile Gln Arg Tyr Ile Tyr Glu Val Glu Gln  
 245 250 255

Gly Leu Tyr Pro Ala Glu Glu His Ser Phe Gln  
 260 265

<210> 9  
 <211> 349  
 <212> PRT  
 <213> *Aspergillus nidulans*

<400> 9

Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg  
 1 5 10 15

Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His  
 20 25 30

Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His  
 35 40 45

Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys  
 50 55 60

Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Lys Gly Glu Pro Ile  
 65 70 75 80

Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala  
 85 90 95

Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala  
 100 105 110

Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val  
 115 120 125

His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser  
 130 135 140

Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln  
 145 150 155 160

Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu  
 165 170 175

Glu Gly Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala  
 180 185 190

Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn  
 195 200 205

Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu  
 210 215 220

Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met  
 225 230 235 240

Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln  
 245 250 255

Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser  
 260 265 270

Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly  
275 280 285

Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu  
290 295 300

Ala Leu Gln Gly Ile Gln Gln Tyr Arg Glu Glu Val Lys Ser Arg Ala  
305 310 315 320

Tyr Pro Ala Glu Gln His Thr Tyr Pro Ile Pro Lys Glu Glu Leu Val  
325 330 335

Glu Phe Gln Lys Ala Val Asp Glu Leu Pro Glu Glu Lys  
340 345

<210> 10

<211> 347

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Ala Ser Ser Leu Thr Arg Asn Cys Ser Arg Phe Ser Lys Ala Ile  
1 5 10 15

Ser Val Arg Phe Met Ser Asn Leu Pro Glu Asn Thr Val Tyr Gly Gly  
20 25 30

Pro Lys Pro Gln Asn Pro Asn Gln Arg Val Thr Leu Thr His Leu Arg  
35 40 45

Gln Lys His Arg Arg Gly Glu Pro Ile Thr Val Val Thr Ala Tyr Asp  
50 55 60

Tyr Pro Ser Ala Val His Leu Asp Thr Ala Gly Ile Asp Val Cys Leu  
65 70 75 80

Val Gly Asp Ser Ala Ser Met Val Val His Gly His Asp Thr Thr Leu  
85 90 95

Pro Ile Ser Leu Asp Glu Met Leu Val His Cys Arg Ala Val Ala Arg  
100 105 110

Gly Ala Lys Arg Pro Leu Leu Val Gly Asp Leu Pro Phe Gly Thr Tyr  
115 120 125

Glu Ser Ser Ser Ser Gln Ala Val Asp Thr Ala Val Arg Val Leu Lys  
130 135 140

Glu Gly Gly Met Asp Ala Ile Lys Leu Glu Gly Gly Ser Ala Ser Arg  
145 150 155 160

Ile Thr Ala Ala Lys Ala Ile Val Glu Ala Gly Ile Ala Val Ile Gly  
165 170 175

His Val Gly Leu Thr Pro Gln Ala Ile Ser Val Leu Gly Gly Phe Arg  
180 185 190

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Pro Gln Gly Arg Asn Ile Ala Ser Ala Val Lys Val Val Glu Thr Ala  
 195 200 205

Met Ala Leu Gln Glu Ala Gly Cys Phe Ser Val Val Leu Glu Cys Val  
 210 215 220

Pro Pro Pro Val Ala Ala Ala Ala Thr Ser Ala Leu Lys Ile Pro Thr  
 225 230 235 240

Ile Gly Ile Gly Ala Gly Pro Phe Cys Ser Gly Gln Val Leu Val Tyr  
 245 250 255

His Asp Leu Leu Gly Met Met Gln His Pro His His Ala Lys Val Thr  
 260 265 270

Pro Lys Phe Cys Lys Gln Tyr Ala Asn Val Gly Glu Val Ile Asn Lys  
 275 280 285

Ala Leu Met Glu Tyr Lys Glu Glu Val Ser Lys Lys Val Phe Pro Gly  
 290 295 300

Pro Ser His Ser Pro Tyr Lys Ile Thr Ala Ser Glu Leu Asp Gly Phe  
 305 310 315 320

Leu Thr Glu Leu Gln Lys Leu Gly Phe Asp Lys Ala Ala Ser Ala Ala  
 325 330 335

Ala Leu Ala Ala Glu Asn Met Glu Pro Ser Lys  
 340 345

<210> 11  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 11  
 Met Asn Ile Met Lys Arg Gln Leu Cys Thr Ser Ser Lys Arg Phe Phe  
 1 5 10 15

Ser Thr Ala Lys Asn Val Val Lys Tyr Asn Thr Ile Gln Asp Ile Arg  
 20 25 30

Asn Lys Tyr Phe Thr Gly Thr Pro Leu Ser Met Cys Thr Ala Tyr Asp  
 35 40 45

Phe Ile Thr Ala Thr Trp Val Asn Lys Ala Asn Cys Asp Leu Leu Leu  
 50 55 60

Val Gly Asp Ser Leu Ala Met Thr Ser Leu Gly Tyr Asp Ser Thr Ile  
 65 70 75 80

Thr Leu Ser Leu Asn Glu Phe Lys Tyr His Val Ala Ser Val Cys Arg  
 85 90 95

Ala Glu Gly Ser Ser Met Val Val Val Asp Met Pro Phe Gly Thr Phe  
 100 105 110

Glu Ser Gly Ile Ser Asp Gly Leu Lys Asn Ala Ile Asp Ile Met Lys  
 115 120 125  
 Leu Asp Ser Lys Val Thr Ser Val Lys Val Glu Val Gly Ser Tyr Thr  
 130 135 140  
 Lys Asp Lys Tyr Ala Met Lys Phe Ile Glu Glu Leu Cys Ser Arg Gly  
 145 150 155 160  
 Ile Pro Val Met Ala His Ile Gly Leu Thr Pro Gln Lys Val His Ser  
 165 170 175  
 Leu Gly Gly Tyr Lys Val Gln Gly Ser Lys Ser Leu Leu Gln Met Gln  
 180 185 190  
 Glu Leu Tyr Glu Thr Ala Met Gln Leu Gln Lys Ile Gly Cys Trp Ser  
 195 200 205  
 Ile Leu Ile Glu Cys Val Pro His Lys Met Ala Gln Phe Ile Thr Ser  
 210 215 220  
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Thr Ser  
 225 230 235 240  
 Gly Gln Val Leu Val Ile Ser Asp Leu Leu Gly Met Gln Gly Asp Ser  
 245 250 255  
 Val Pro Lys Phe Val Lys Gln Ala Val Asn Met Thr Asp Ile Ala Thr  
 260 265 270  
 Gln Gly Leu Lys Glu Tyr Ile Ala Ser Val Glu Asp Arg Thr Phe Pro  
 275 280 285  
 Glu Arg Gly Thr His Thr Phe Lys Val Lys Glu Asp Leu Trp Asn Glu  
 290 295 300  
 Phe Leu Ser Ser Ile Asn Glu Lys  
 305 310

<210> 12

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

<220>

<221> SITE

<222> 1..4, 6..8, 10..22, 27..29, 31..39, 41, 50..52, 54..56

<223> Xaa is uncertain

<220>

<221> SITE

<222> 59, 62..64, 66, 67, 69..71, 73, 76..81, 83, 88, 89

<223> Xaa is uncertain

COPY

<220>  
<221> SITE  
<222> 91..96, 97..100, 102, 103, 105..108, 110..113, 120..133  
<223> Xaa is uncertain

<220>  
<221> SITE  
<222> 135..138, 140, 142, 145, 151..155, 163, 165..171  
<223> Xaa is uncertain

<220>  
<221> SITE  
<222> 173..175, 177, 179..181, 185, 186, 191, 194, 195  
<223> Xaa is uncertain

<220>  
<221> SITE  
<222> 198..200, 202..205, 208, 215..217, 224, 225, 227, 228  
<223> Xaa is uncertain

<220>  
<221> SITE  
<222> 230..242, 246, 248..258, 260..262, 264..266, 268..271  
<223> Xaa is uncertain

<220>  
<221> SITE  
<222> 274..277, 279..281  
<223> Xaa is uncertain

<400> 12  
Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15  
Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Asp Xaa Xaa Xaa Ala Xaa Xaa  
20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Val Gly Asp Ser Leu Gly  
35 40 45  
Met Xaa Xaa Xaa Gly Xaa Xaa Xaa Thr Leu Xaa Val Thr Xaa Xaa Xaa  
50 55 60  
Ile Xaa Xaa His Xaa Xaa Xaa Val Xaa Arg Gly Xaa Xaa Xaa Xaa Xaa  
65 70 75 80  
Xaa Leu Xaa Asp Leu Pro Phe Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa  
85 90 95  
Ala Xaa Xaa Xaa Ala Xaa Xaa Val Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa  
100 105 110  
Xaa Val Lys Ile Glu Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
115 120 125  
Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Val Xaa Val Xaa Gly His  
130 135 140

COPY

Xaa Gly Leu Thr Pro Gln Xaa Xaa Xaa Xaa Xaa Gly Gly Tyr Lys Val  
 145 150 155 160

Gln Gly Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Ala  
 165 170 175

Xaa Ala Xaa Xaa Xaa Ala Gly Ala Xaa Xaa Leu Val Leu Glu Xaa Val  
 180 185 190

Pro Xaa Xaa Leu Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ile Pro Xaa  
 195 200 205

Ile Gly Ile Gly Ala Gly Xaa Xaa Xaa Asp Gly Gln Ile Leu Val Xaa  
 210 215 220

Xaa Asp Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 225 230 235 240

Xaa Xaa Pro Lys Phe Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 245 250 255

Xaa Xaa Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Tyr  
 260 265 270

Pro Xaa Xaa Xaa Xaa His Xaa Xaa Xaa  
 275 280